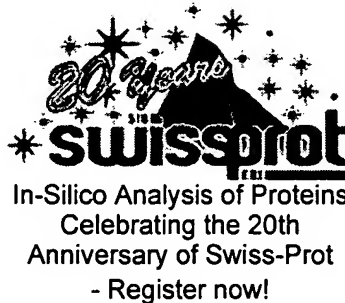


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# UniProtKB/TrEMBL entry Q9FCY5

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## Entry information

Entry name	<b>Q9FCY5_ECOLI</b>
Primary accession number	<b>Q9FCY5</b>
Secondary accession numbers	None
Integrated into TrEMBL on	March 1, 2001
Sequence was last modified on	March 1, 2002 (Sequence version 2)
Annotations were last modified on	February 7, 2006 (Entry version 20)
<b>Name and origin of the protein</b>	
Protein name	<b>Invasion protein IbeA</b>
Synonyms	None
Gene name	None
From	Escherichia coli [TaxID: 562]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

## References

### [1] NUCLEOTIDE SEQUENCE.

PubMed=7591087 [NCBI, ExPASy, EBI, Israel, Japan]

Huang S.H., Wass C., Fu Q., Prasadara N.V., Stins M., Kim K.S.;

"Escherichia coli invasion of brain microvascular endothelial cells in vitro and in vivo: mole cloning and characterization of invasion gene ibe10.";

Infect. Immun. 63:4470-4475(1995).

### [2] NUCLEOTIDE SEQUENCE.

DOI=10.1016/S1286-4579(00)01277-6; PubMed=11008113 [NCBI, ExPASy, EBI, Israel, .

Huang S.H., Stins M.F., Kim K.S.;

"Bacterial penetration across the blood-brain barrier during the development of neonatal meningitis.";

Microbes Infect. 2:1237-1244(2000).

### [3] NUCLEOTIDE SEQUENCE.

DOI=10.1086/319290; PubMed=11237832 [NCBI, ExPASy, EBI, Israel, Japan]  
Huang S.H., Wan Z.S., Chen Y.H., Jong A.Y., Kim K.S.;  
"Further characterization of Escherichia coli brain microvascular endothelial cell invasion by  
ibeA by deletion, complementation, and protein expression.";  
J. Infect. Dis. 183:1071-1078(2001).

#### [4] NUCLEOTIDE SEQUENCE.

DOI=10.1007/s101420100039; PubMed=11793250 [NCBI, ExPASy, EBI, Israel, Japan]  
Huang S.H., Chen Y.H., Kong G., Chen S.H., Besemer J., Borodovsky M., Jong A.;  
"A novel genetic island of meningitic Escherichia coli K1 containing the ibeA invasion gene  
(GimA): functional annotation and carbon-source-regulated invasion of human brain  
microvascular endothelial cells.";  
Funct. Integr. Genomics 1:312-322(2001).

#### Comments

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#### Cross-references

##### Sequence databases

EMBL AF289032; AAF98391.2; -; [EMBL / GenBank / DDBJ]  
Genomic\_DNA. [CoDingSequence]

##### 3D structure databases

ModBase Q9FCY5.

##### 2D gel databases

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##### Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

##### Ontologies

GO GO:0016491; Molecular function: oxidoreductase activity (*inferred from electronic annotation*).  
GO GO:0006118; Biological process: electron transport (*inferred from electronic annotation*).  
QuickGo  
view.

##### Family and domain databases

InterPro IPR004792; HI0933\_like.  
IPR000205; NAD\_BS.  
IPR000103; Pyridine\_redox\_2.  
Graphical view of domain structure.  
Pfam PF03486; HI0933\_like; 1.  
Pfam graphical view of domain structure.  
PRINTS PR00469; PNDRDTASEII.  
ProDom [Domain structure / List of seq. sharing at least 1 domain]

##### Other

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

**Keywords****NAD; Oxidoreductase.****Features**

None

**Sequence information**

Length: **456** Molecular weight: **49772 Da** CRC64: **00FD72D7E9B0E010** [This is a checksum of sequence]

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ESIAWWRHEN TVESGGLARE IEETAKSMGA SSPEPQSNSQ AINEERFKLV ADAMLEQAGV

     130     140     150     160     170     180
RRVLHITAVD VIKQGNNLLG VITESKSGRQ AILANVIIDC TGDADIAWFA GAPFIKRERE

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ELMCMTTVFS CANINKNAFM QNINSTEPKY GDWGADEENK NWSYDVHESC RDMFSPYL GK

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VLRKERSAGI IPKDVTLGGS WSTVTEYGDA NYLNVVSIPA VDCTDVFDLT RAEIEGRKQA

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MQAIEALRQF QPGFEQAQLK NFGMTVGTRE SRHIIGRVQL TENDICNEGR HADSIGVFPE

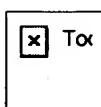
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     430     440     450
GAGTAAAI AI KNNTTVSQVD IQTVQERLQQ NGVKVF

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FEMS Microbiol Lett. 1996 Nov 1;144(2-3):171-6.

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**Mapping of noninvasion TnphoA mutations on the Escherichia coli O18:K1:H7 chromosome.**

**Bloch CA, Huang SH, Rode CK, Kim KS.**

Department of Pediatrics and Epidemiology, University of Michigan, Ann Arbor 48109-0656, USA.

The most virulent newborn meningitis-associated Escherichia coli are of the serotype O18:K1:H7. We previously isolated a large number of E. coli O18:K1:H7 mutants resulting from transposon TnphoA mutagenesis that fail to invade brain microvascular endothelial cells. We have now determined 45 independent insertions. Twelve were localized to the 98 min region, containing a 120 kb segment that is characteristic of E. coli O18:K1:H7. Another, the previously described insertion ibe-10::TnphoA, was localized to the 87 min region, containing a 20 kb segment found in this E. coli. These noninvasion mutations may define new O18:K1:H7 pathogenicity islands carrying genes for penetration of the blood-brain barrier of newborn mammals.

PMID: 8900061 [PubMed - indexed for MEDLINE]

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